

**XP-002249761**

**AN - 2003-342454 [32]**

**AP - WO2002JP08448 20020822**

**CPY - CIRC-N**

**DC - B04 D16**

**DS - BE CY EA FR GR IE IT MC NL OA SZ**

**DR - 1857-U 2044-U**

**FS - CPI**

**IC - C12N15/09 ; C12Q1/68**

**IN - MARUYAMA A**

**MC - B04-C02C B04-C03C B04-E01 B04-E05 B04-E09 B04-N04 B05-B01P B11-C08E5  
B12-K04A B12-K04E B12-K04F D05-H09 D05-H12D1 D05-H18A**

**M1 - [01] M417 M423 M781 M905 P831 Q232 Q233; RA00I9-K RA00I9-U**

**- [02] H1 H101 H182 J0 J011 J1 J171 M280 M315 M321 M332 M343 M349 M381  
M391 M416 M423 M620 M781 M904 M905 P831 Q232 Q233; RA030X-K RA030X-U**

**- [03] H4 H402 H482 H5 H589 H8 M280 M312 M323 M332 M342 M383 M393 M423  
M510 M520 M530 M540 M620 M781 M904 M905 M910 P831 Q232 Q233; R02044-K  
R02044-U; 2044-U**

**- [04] M423 M781 M904 M905 M910 P831 Q232 Q233; R01857-K R01857-U  
R16573-K R16573-U; 1857-U**

**- [05] B415 B702 B713 B720 B815 B833 H181 H182 H183 H401 H402 H403 H404  
H405 H481 H482 H483 H484 H7 H725 J011 J012 J013 J271 J272 J273 L640  
L660 L699 M210 M211 M212 M213 M214 M215 M216 M220 M221 M222 M223 M224  
M231 M232 M233 M272 M273 M280 M281 M282 M283 M311 M312 M313 M314 M315  
M316 M321 M322 M323 M331 M332 M333 M334 M340 M342 M343 M344 M361 M381  
M383 M391 M393 M411 M423 M510 M520 M530 M540 M781 M904 M905 P831 Q232  
Q233; 0091-04901-K 0091-04901-U**

**- [06] M423 M750 M905 N102 P831 Q232 Q233; RA00NS-K RA00NS-A**

**- [07] M423 M750 M905 N102 P831 Q232 Q233; RA012P-K RA012P-A**

**M6 - [08] M905 P831 Q232 Q233 R160 R501 R515 R521 R627 R639**

**PA - (CIRC-N) CIRCLE PROMOTION SCI & ENG**

**PN - WO03018841 A1 20030306 DW200332 C12Q1/68 Jpn 044pp**

**PR - JP20010253789 20010824**

**XA - C2003-089827**

**XIC - C12N-015/09 ; C12Q-001/68**

**AB - WO2003018841 NOVELTY - Judgement of mismatch between single-stranded  
nucleic acid molecules of a sample and a standard, comprises:**

- (a) mixing a specific double-stranded nucleic acid molecule with a  
cationic polymer; and**
- (b) measuring speed or ratio of the substitution of the sample  
single-stranded nucleic acid molecule by the complementary strand of  
the standard single-stranded nucleic acid molecule.**
- DETAILED DESCRIPTION - Judgement of mismatch (M1) between  
single-stranded nucleic acid molecules of a sample and a standard  
comprises:**
  - (a) allowing a double-stranded nucleic acid molecule consisting of the  
standard single-stranded nucleic acid molecule with its complementary  
strand to coexist with the sample single-stranded nucleic acid  
molecule in the presence of a cationic polymer; and**
  - (b) measuring speed or ratio of the substitution of the sample  
single-stranded nucleic acid molecule by the complementary strand of  
the standard single-stranded nucleic acid molecule.**

**AN INDEPENDENT CLAIM is also included for a method (M2) in which**

either:

- (a) the sample and standard single-stranded nucleic acid molecules are brought into contact to form a double-stranded nucleic acid molecule;
  - (b) allowing the thus formed double-stranded nucleic acid molecule to coexist with the totally complementary strand of the standard single-stranded nucleic acid in the presence of a cationic polymer; and
  - (c) measuring speed or ratio of the substitution of the sample single-stranded nucleic acid molecule by the totally complementary strand of the standard single-stranded nucleic acid molecule; or
  - (d) a double-stranded nucleic acid molecule consisting of the standard single-stranded nucleic acid molecule with its totally complementary strand is allowed to coexist with the sample single-stranded nucleic acid molecule in the presence of a cationic polymer; and
  - (e) calculation of the formation ratio of double-stranded nucleic acid molecules containing the standard single-stranded nucleic acid molecule and its totally complementary strand, and the double-stranded nucleic acid molecule containing the standard single-stranded nucleic acid molecule and the sample single-stranded nucleic acid molecule.
- USE - The method is applicable in locating single nucleotide polymorphism, DNA analysis and disease diagnosis.

- (Dwg.0/7)

CN - RA00I9-K RA00I9-U RA030X-K RA030X-U R02044-K R02044-U R01857-K  
R01857-U R16573-K R16573-U 0091-04901-K 0091-04901-U RA00NS-K RA00NS-A  
RA012P-K RA012P-A

DN - AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM  
DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC  
LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD  
SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

DRL - 2044-U 1857-U

IW - JUDGEMENT MISMATCH SINGLE STRAND NUCLEIC ACID MOLECULAR APPLY LOCATE  
SINGLE NUCLEOTIDE POLYMORPH DNA ANALYSE DISEASE DIAGNOSE CATION  
POLYMER MEDIATOR

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SINGLE NUCLEOTIDE POLYMORPH DNA ANALYSE DISEASE DIAGNOSE CATION  
POLYMER MEDIATOR

INW - MARUYAMA A

NC - 101

OPD - 2001-08-24

ORD - 2003-03-06

PAW - (CIRC-N) CIRCLE PROMOTION SCI & ENG

TI - Judgement of mismatch between single-stranded nucleic acid molecules,  
applicable in locating single nucleotide polymorphism, DNA analysis  
and disease diagnosis, is cationic polymer-mediated